

FIG. 1A

Met	Leu	Ala	Arg	Ala	Leu	Leu	Leu	Cys	Ala	Val	Leu	Ala	Leu	Ser	His	1	5	10	15
Thr	Ala	Asn	Pro	Cys	Cys	Ser	His	Pro	Cys	Gln	Asn	Arg	Gly	Val	Cys	20	25	30	
Met	Ser	Val	Gly	Phe	Asp	Gln	Tyr	Lys	Cys	Asp	Cys	Thr	Arg	Thr	Gly	35	40	45	
Phe	Tyr	Gly	Glu	Asn	Cys	Ser	Thr	Pro	Glu	Phe	Leu	Thr	Arg	Ile	Lys	50	55	60	
Leu	Phe	Leu	Lys	Pro	Thr	Pro	Asn	Thr	Val	His	Tyr	Ile	Leu	Thr	His	65	70	75	80
Phe	Lys	Gly	Phe	Trp	Asn	Val	Val	Asn	Asn	Ile	Pro	Phe	Leu	Arg	Asn	85	90	95	
Ala	Ile	Met	Ser	Tyr	Val	Leu	Thr	Ser	Arg	Ser	His	Leu	Ile	Asp	Ser	100	105	110	
Pro	Pro	Thr	Tyr	Asn	Ala	Asp	Tyr	Gly	Tyr	Lys	Ser	Trp	Glu	Ala	Phe	115	120	125	
Ser	Asn	Leu	Ser	Tyr	Tyr	Thr	Arg	Ala	Leu	Pro	Pro	Val	Pro	Asp	Asp	130	135	140	
Cys	Pro	Thr	Pro	Leu	Gly	Val	Lys	Gly	Lys	Lys	Gln	Leu	Pro	Asp	Ser	145	150	155	160
Asn	Glu	Ile	Val	Glu	Lys	Leu	Leu	Leu	Arg	Arg	Lys	Phe	Ile	Pro	Asp	165	170	175	
Pro	Gln	Gly	Ser	Asn	Met	Met	Phe	Ala	Phe	Phe	Ala	Gln	His	Phe	Thr	180	185	190	
His	Gln	Phe	Phe	Lys	Thr	Asp	His	Lys	Arg	Gly	Pro	Ala	Phe	Thr	Asn	195	200	205	
Gly	Leu	Gly	His	Gly	Val	Asp	Leu	Asn	His	Ile	Tyr	Gly	Glu	Thr	Leu	210	215	220	
Ala	Arg	Gln	Arg	Lys	Leu	Arg	Leu	Phe	Lys	Asp	Gly	Lys	Met	Lys	Tyr	225	230	235	240
Gln	Ile	Ile	Asp	Gly	Glu	Met	Tyr	Pro	Pro	Thr	Val	Lys	Asp	Thr	Gln	245	250	255	
Ala	Glu	Met	Ile	Tyr	Pro	Pro	Gln	Val	Pro	Glu	His	Leu	Arg	Phe	Ala	260	265	270	
Val	Gly	Gln	Glu	Val	Phe	Gly	Leu	Val	Pro	Gly	Leu	Met	Met	Tyr	Ala	275	280	285	
Thr	Ile	Trp	Leu	Arg	Glu	His	Asn	Arg	Val	Cys	Asp	Val	Leu	Lys	Gln	290	295	300	

FIG. 1B

Glu His Pro Glu Trp Gly Asp Glu Gln Leu Phe Gln Thr Ser Arg Leu
305 310 315 320

Ile Leu Ile Gly Glu Thr Ile Lys Ile Val Ile Glu Asp Tyr Val Gln
325 330 335

His Leu Ser Gly Tyr His Phe Lys Leu Lys Phe Asp Pro Glu Leu Leu
340 345 350

Phe Asn Lys Gln Phe Gln Tyr Gln Asn Arg Ile Ala Ala Glu Phe Asn
355 360 365

Thr Leu Tyr His Trp His Pro Leu Leu Pro Asp Thr Phe Gln Ile His
370 375 380

Asp Gln Lys Tyr Asn Tyr Gln Gln Phe Ile Tyr Asn Asn Ser Ile Leu
385 390 395 400

Leu Glu His Gly Ile Thr Gln Phe Val Glu Ser Phe Thr Arg Gln Ile
405 410 415

Ala Gly Arg Val Ala Gly Gly Arg Asn Val Pro Pro Ala Val Gln Lys
420 425 430

Val Ser Gln Ala Ser Ile Asp Gln Ser Arg Gln Met Lys Tyr Gln Ser
435 440 445

Phe Asn Glu Tyr Arg Lys Arg Phe Met Leu Lys Pro Tyr Glu Ser Phe
450 455 460

Glu Glu Leu Thr Gly Glu Lys Glu Met Ser Ala Glu Leu Glu Ala Leu
465 470 475 480

Tyr Gly Asp Ile Asp Ala Val Glu Leu Tyr Pro Ala Leu Leu Val Glu
485 490 495

Lys Pro Arg Pro Asp Ala Ile Phe Gly Glu Thr Met Val Glu Val Gly
500 505 510

Ala Pro Phe Ser Leu Lys Gly Leu Met Gly Asn Val Ile Cys Ser Pro
515 520 525

Ala Tyr Trp Lys Pro Ser Thr Phe Gly Gly Glu Val Gly Phe Gln Ile
530 535 540

Ile Asn Thr Ala Ser Ile Gln Ser Leu Ile Cys Asn Asn Val Lys Gly
545 550 555 560

Cys Pro Phe Thr Ser Phe Ser Val Pro Asp Pro Glu Leu Ile Lys Thr
565 570 575

Val Thr Ile Asn Ala Ser Ser Ser Arg Ser Gly Leu Asp Asp Ile Asn
580 585 590

Pro Thr Val Leu Leu Lys Glu Arg Ser Thr Glu Leu (SEQ ID NO: 10)
595 600

FIG. 2A

GTCCAGGAAC	TCCTCAGCAG	CGCCTCCTTC	AGCTCCACAG	CCAGACGCCC	TCAGACAGCA	60
AAGCCTACCC	CCGCGCCGCG	CCCTGCCCCG	CGCTGCGATG	CTCGCCCGCG	CCCTGCTGCT	120
GTGCGCGGTC	CTGGCGCTCA	GCCATACAGC	AAATCCTTGC	TGTTCCCACC	CATGTCAAAA	180
CCGAGGTGTA	TGTATGAGTG	TGGGATTGTA	CCAGTATAAG	TGCGATTGTA	CCCGGACAGG	240
ATTCTATGGA	GAAAACTGCT	CAACACCGGA	ATTTTTGACA	AGAATAAAAT	TATTTCTGAA	300
ACCCACTCCA	AACACAGTGC	ACTACATACT	TACCCACTTC	AAGGGATTTT	GGAACGTTGT	360
GAATAACATT	CCCTTCCTTC	GAAATGCAAT	TATGAGTTAT	GTGTTGACAT	CCAGATCACA	420
TTTGATTGAC	AGTCCACCAA	CTTACAATGC	TGACTATGGC	TACAAAAGCT	GGGAAGCCTT	480
CTCTAACCTC	TCCTATTATA	CTAGAGCCCT	TCCTCCTGTG	CCTGATGATT	GCCCGACTCC	540
CTTGGGTGTC	AAAGGTAAAA	AGCAGCTTCC	TGATTCAAAT	GAGATTGTGG	AAAAATTGCT	600
TCTAAGAAGA	AAGTTCATCC	CTGATCCCCA	GGGCTCAAAC	ATGATGTTTG	CATTCCTTGC	660
CCAGCACTTC	ACGCACCAGT	TTTTCAAGAC	AGATCATAAG	CGAGGGCCAG	CTTTCACCAA	720
CGGGCTGGGC	CATGGGGTGG	ACTTAAATCA	TATTTACGGT	GAAACTCTGG	CTAGACAGCG	780
TAAACTGCGC	CTTTTCAAGG	ATGGAAAAAT	GAAATATCAG	ATAATTGATG	GAGAGATGTA	840
TCCTCCCACA	GTCAAAGATA	CTCAGGCAGA	GATGATCTAC	CCTCCTCAAG	TCCCTGAGCA	900
TCTACGGTTT	GCTGTGGGGC	AGGAGGTCTT	TGGTCTGGTG	CCTGGTCTGA	TGATGTATGC	960
CACAATCTGG	CTGCGGGAAC	ACAACAGAGT	ATGTGATGTG	CTTAAACAGG	AGCATCCTGA	1020
ATGGGGTGAT	GAGCAGTTGT	TCCAGACAAG	CAGGCTAATA	CTGATAGGAG	AGACTATTAA	1080
GATTGTGATT	GAAGATTATG	TGCAACACTT	GAGTGGCTAT	CACTTCAAAC	TGAAATTTGA	1140
CCCAGAACTA	CTTTTCAACA	AACAATTCCA	GTACCAAAAT	CGTATTGCTG	CTGAATTTAA	1200
CACCTCTAT	CACTGGCATC	CCCTTCTGCC	TGACACCTTT	CAAATTCATG	ACCAGAAATA	1260
CAACTATCAA	CAGTTTATCT	ACAACAATC	TATATTGCTG	GAACATGGAA	TTACCCAGTT	1320
TGTTGAATCA	TTCACCAGGC	AAATTGCTGG	CAGGGTTGCT	GGTGGTAGGA	ATGTTCCACC	1380
CGCAGTACAG	AAAGTATCAC	AGGCTTCCAT	TGACCAGAGC	AGGCAGATGA	AATACCAGTC	1440
TTTTAATGAG	TACCGCAAAC	GCTTTATGCT	GAAGCCCTAT	GAATCATTTG	AAGAACTTAC	1500
AGGAGAAAAG	GAAATGTCTG	CAGAGTTGGA	AGCACTCTAT	GGTGACATCG	ATGCTGTGGA	1560
GCTGTATCCT	GCCCTTCTGG	TAGAAAAGCC	TCGGCCAGAT	GCCATCTTTG	GTGAAACCAT	1620
GGTAGAAGTT	GGAGCACCAT	TCTCCTTGAA	AGGACTTATG	GGTAATGTTA	TATGTTCTCC	1680
TGCCTACTGG	AAGCCAAGCA	CTTTTGGTGG	AGAAGTGGGT	TTTCAAATCA	TCAACACTGC	1740

FIG. 2B

CTCAATTCAG	TCTCTCATCT	GCAATAACGT	GAAGGGCTGT	CCCTTTACTT	CATTCAGTGT	1800
TCCAGATCCA	GAGCTCATTA	AAACAGTCAC	CATCAATGCA	AGTTCTTCCC	GCTCCGGACT	1860
AGATGATATC	AATCCCACAG	TACTACTAAA	AGAACGGTCG	ACTGAACTGT	AGAAGTCTAA	1920
TGATCATATT	TATTTATTTA	TATGAACCAT	GTCTATTAAT	TTAATTATTT	AATAATATTT	1980
ATATTAAACT	CCTTATGTTA	CTTAACATCT	TCTGTAACAG	AAGTCAGTAC	TCCTGTTGCG	2040
GAGAAAGGAG	TCATACTTGT	GAAGACTTTT	ATGTCACTAC	TCTAAAGATT	TTGCTGTTGC	2100
TGTTAAGTTT	GGAAAACAGT	TTTTATTCTG	TTTTATAAAC	CAGAGAGAAA	TGAGTTTGA	2160
CGTCTTTTTA	CTTGAATTTC	AACTTATATT	ATAAGGACGA	AAGTAAAGAT	GTTTGAATAC	2220
TTAAACACTA	TCACAAGATG	CCAAAATGCT	GAAAGTTTTT	ACACTGTCGA	TGTTTCCAAT	2280
GCATCTTCCA	TGATGCATTA	GAAGTAACTA	ATGTTTGAAA	TTTTTAAAGTA	CTTTTGGGTA	2340
TTTTTCTGTC	ATCAAAACAAA	ACAGGTATCA	GTGCATTATT	AAATGAATAT	TTAAATTAGA	2400
CATTACCAGT	AATTTTCATGT	CTACTTTTTA	AAATCAGCAA	TGAAACAATA	ATTTGAAATT	2460
TCTAAATTCA	TAGGGTAGAA	TCACCTGTAA	AAGCTTGTTT	GATTTCTTAA	AGTTATTAAA	2520
CTTGTAACATA	TACCAAAAAG	AAGCTGTCTT	GGATTTAAAT	CTGTAAAATC	AGATGAAATT	2580
TTACTACAAT	TGCTTGTTAA	AATATTTTAT	AAGTGATGTT	CCTTTTTTCAC	CAAGAGTATA	2640
AACCTTTTTA	GTGTGACTGT	TAAAACTTCC	TTTTTAAATCA	AAATGCCAAA	TTTATTAAGG	2700
TGGTGGAGCC	ACTGCAGTGT	TATCTCAAAA	TAAGAATATC	CTGTTGAGAT	ATTCCAGAAT	2760
CTGTTTATAT	GGCTGGTAAC	ATGTAAAAAC	CCCATAACCC	CGCCAAAAGG	GGTCCTACCC	2820
TTGAACATAA	AGCAATAACC	AAAGGAGAAA	AGCCCAAATT	ATTGGTTCCA	AATTTAGGGT	2880
TTAAACTTTT	TGAAGCAAAC	TTTTTTTTTAG	CCTTGTCAC	TGCAGACCTG	GTACTCAGAT	2940
TTTGCTATGA	GGTTAATGAA	GTACCAAGCT	GTGCTTGAAT	AACGATATGT	TTTCTCAGAT	3000
TTTCTGTTGT	ACAGTTTAAT	TTAGCAGTCC	ATATCACATT	GCAAAAGTAG	CAATGACCTC	3060
ATAAAATACC	TCTTCAAAAT	GCTTAAATTC	ATTTACACACA	TTAATTTTAT	CTCAGTCTTG	3120
AAGCCAATTC	AGTAGGTGCA	TTGGAATCAA	GCCTGGCTAC	CTGCATGCTG	TTCCTTTTCT	3180
TTTCTTCTTT	TAGCCATTTT	GCTAAGAGAC	ACAGTCTTCT	CAAACACTTC	GTTTCTCCTA	3240
TTTTGTTTTA	CTAGTTTTAA	GATCAGAGTT	CACTTTCTTT	GGACTCTGCC	TATATTTTCT	3300
TACCTGAAC	TTTGCAAGTT	TTCAGGTAAA	CCTCAGCTCA	GGACTGCTAT	TTAGCTCCTC	3360
TTAAGAAGAT	TAATAAAAAA	AAAAAAG	(SEQ ID NO: 11)			3387

Annotated Sheets Showing Changes

FIG. 1A

Met	Leu	Ala	Arg	Ala	Leu	Leu	Leu	Cys	Ala	Val	Leu	Ala	Leu	Ser	His
1				5					10					15	
Thr	Ala	Asn	Pro	Cys	Cys	Ser	His	Pro	Cys	Gln	Asn	Arg	Gly	Val	Cys
	20					25					30				
Met	Ser	Val	Gly	Phe	Asp	Gln	Tyr	Lys	Cys	Asp	Cys	Thr	Arg	Thr	Gly
	35					40						45			
Phe	Tyr	Gly	Glu	Asn	Cys	Ser	Thr	Pro	Glu	Phe	Leu	Thr	Arg	Ile	Lys
	50					55					60				
Leu	Phe	Leu	Lys	Pro	Thr	Pro	Asn	Thr	Val	His	Tyr	Ile	Leu	Thr	His
65					70					75					80
Phe	Lys	Gly	Phe	Trp	Asn	Val	Val	Asn	Asn	Ile	Pro	Phe	Leu	Arg	Asn
				85				90	<u>90</u>					95	
Ala	Ile	Met	Ser	Tyr	Val	Leu	Thr	Ser	Arg	Ser	His	Leu	Ile	Asp	Ser
			100					105					110		
Pro	Pro	Thr	Tyr	Asn	Ala	Asp	Tyr	Gly	Tyr	Lys	Ser	Trp	Glu	Ala	Phe
		115					120					125			
Ser	Asn	Leu	Ser	Tyr	Tyr	Thr	Arg	Ala	Leu	Pro	Pro	Val	Pro	Asp	Asp
	130					135					140				
Cys	Pro	Thr	Pro	Leu	Gly	Val	Lys	Gly	Lys	Lys	Gln	Leu	Pro	Asp	Ser
145					150					155					160
Asn	Glu	Ile	Val	Glu	Lys	Leu	Leu	Leu	Arg	Arg	Lys	Phe	Ile	Pro	Asp
				165					170				175		
Pro	Gln	Gly	Ser	Asn	Met	Met	Phe	Ala	Phe	Phe	Ala	Gln	His	Phe	Thr
			180				185						190		
His	Gln	Phe	Phe	Lys	Thr	Asp	His	Lys	Arg	Gly	Pro	Ala	Phe	Thr	Asn
	195						200					205			
Gly	Leu	Gly	His	Gly	Val	Asp	Leu	Asn	His	Ile	Tyr	Gly	Glu	Thr	Leu
	210					215					220				
Ala	Arg	Gln	Arg	Lys	Leu	Arg	Leu	Phe	Lys	Asp	Gly	Lys	Met	Lys	Tyr
225					230					235					240
Gln	Ile	Ile	Asp	Gly	Glu	Met	Tyr	Pro	Pro	Thr	Val	Lys	Asp	Thr	Gln
				245					250					255	
Ala	Glu	Met	Ile	Tyr	Pro	Pro	Gln	Val	Pro	Glu	His	Leu	Arg	Phe	Ala
			260					265					270		
Val	Gly	Gln	Glu	Val	Phe	Gly	Leu	Val	Pro	Gly	Leu	Met	Met	Tyr	Ala
	275						280					285			
Thr	Ile	Trp	Leu	Arg	Glu	His	Asn	Arg	Val	Cys	Asp	Val	Leu	Lys	Gln
	290					295					300				

• •

• •

FIG. 1B

FIG. 1B

Asp	Glu	Gln	Leu	Phe	Gln	Thr	Ser	Arg	Leu
				315					320
Ile	Lys	Ile	Val	Ile	Glu	Asp	Tyr	Val	Gln
			330					335	
Phe	Lys	Leu	Lys	Phe	Asp	Pro	Glu	Leu	Leu
		345					350		
Tyr	Gln	Asn	Arg	Ile	Ala	Ala	Glu	Phe	Asn
	360					365			
Pro	Leu	Leu	Pro	Asp	Thr	Phe	Gln	Ile	His
375					380				
Gln	Gln	Phe	Ile	Tyr	Asn	Asn	Ser	Ile	Leu
				395					400
Gln	Phe	Val	Glu	Ser	Phe	Thr	Arg	Gln	Ile
			410					415	
Gly	Arg	Asn	Val	Pro	Pro	Ala	Val	Gln	Lys
		425					430		
Asp	Gln	Ser	Arg	Gln	Met	Lys	Tyr	Gln	Ser
	440					445			
Arg	Phe	Met	Leu	Lys	Pro	Tyr	Glu	Ser	Phe
455					460				
Lys	Glu	Met	Ser	Ala	Glu	Leu	Glu	Ala	Leu
				475					480
Val	Glu	Leu	Tyr	Pro	Ala	Leu	Leu	Val	Glu
			490					495	
Ile	Phe	Gly	Glu	Thr	Met	Val	Glu	Val	Gly
		505					510		
Gly	Leu	Met	Gly	Asn	Val	Ile	Cys	Ser	Pro
	520					525			
Thr	Phe	Gly	Gly	Glu	Val	Gly	Phe	Gln	Ile
535					540				
Gln	Ser	Leu	Ile	Cys	Asn	Asn	Val	Lys	Gly
				555					560
Ser	Val	Pro	Asp	Pro	Glu	Leu	Ile	Lys	Thr
			570					575	
Ser	Ser	Arg	Ser	Gly	Leu	Asp	Asp	Ile	Asn
		585					590		
Glu	Arg	Ser	Thr	Glu	Leu	(SEQ ID NO: 10)			
	600								

Annotated Sheets Showing Changes

FIG. 2A

GTCCAGGAAC	TCCTCAGCAG	CGCCTCCTTC	AGCTCCACAG	CCAGACGCCC	TCAGACAGCA	60
AAGCCTACCC	CCGCGCCGCG	CCCTGCCCCG	CGCTGCGATG	CTCGCCCGCG	CCCTGCTGCT	120
GTGCGCGGTC	CTGGCGCTCA	GCCATACAGC	AAATCCTTGC	TGTTCCCACC	CATGTCAAAA	180
CCGAGGTGTA	TGTATGAGTG	TGGGATTTGA	CCAGTATAAG	TGCGATTGTA	CCCGGACAGG	240
ATTCTATGGA	GAAAAC TGCT	CAACACCGGA	ATTTTTGACA	AGAATAAAAT	TATTTCTGAA	300
ACCCACTCCA	AACACAGTGC	ACTACATACT	TACCCACTTC	AAGGGATTTT	GGAACGTTGT	360
GAATAACATT	CCCTTCCTTC	GAAATGCAAT	TATGAGTTAT	GTGTTGACAT	CCAGATCACA	420
TTTGATTGAC	AGTCCACCAA	CTTACAATGC	TGACTATGGC	TACAAAAGCT	GGGAAGCCTT	480
CTCTAACCTC	TCCTATTATA	CTAGAGCCCT	TCCTCCTGTG	CCTGATGATT	GCCCCACTCC	540
CTTGGGTGTC	AAAGGTAAAA	AGCAGCTTCC	TGATTCAAAT	GAGATTGTGG	AAAAATTGCT	600
TCTAAGAAGA	AAGTTCATCC	CTGATCCCCA	GGGCTCAAAC	ATGATGTTTG	CATTCTTTGC	660
CCAGCACTTC	ACGCACCAGT	TTTTCAAGAC	AGATCATAAG	CGAGGGCCAG	CTTTCACCAA	720
CGGGCTGGGC	CATGGGGTGG	ACTTAAATCA	TATTTACGGT	GAAACTCTGG	CTAGACAGCG	780
TAAACTGCGC	CTTTTCAAGG	ATGGAAAAAT	GAAATATCAG	ATAATTGATG	GAGAGATGTA	840
TCCTCCCACA	GTCAAAGATA	CTCAGGCAGA	GATGATCTAC	CCTCCTCAAG	TCCCTGAGCA	900
TCTACGGTTT	GCTGTGGGGC	AGGAGGTCTT	TGGTCTGGTG	CCTGGTCTGA	TGATGTATGC	960
CACAATCTGG	CTGCGGGAAC	ACAACAGAGT	ATGTGATGTG	CTTAAACAGG	AGCATCCTGA	1020
ATGGGGTGAT	GAGCAGTTGT	TCCAGACAAG	CAGGCTAATA	CTGATAGGAG	AGACTATTAA	1080
GATTGTGATT	GAAGATTATG	TGCAACACTT	GAGTGGCTAT	CACTTCAAAC	TGAAATTTGA	1140
CCCAGAACTA	CTTTTCAACA	AACAATTCCA	GTACCAAAAT	CGTATTGCTG	CTGAATTTAA	1200
CACCCTCTAT	CACTGGCATC	CCCTTCTGCC	TGACACCTTT	CAAATTCATG	ACCAGAAATA	1260
CAACTATCAA	CAGTTTATCT	ACAACAATC	TATATTGCTG	GAACATGGAA	TTACCCAGTT	1320
TGTTGAATCA	TTCACCAGGC	AAATTGCTGG	CAGGGTTGCT	GGTGGTAGGA	ATGTTCCACC	1380
CGCAGTACAG	AAAGTATCAC	AGGCTTCCAT	TGACCAGAGC	AGGCAGATGA	AATACCAGTC	1440
TTTTAATGAG	TACCGCAAAC	GCTTTATGCT	GAAGCCCTAT	GAATCATTTG	AAGAACTTAC	1500
AGGAGAAAAG	GAAATGTCTG	CAGAGTTGGA	AGCACTCTAT	GGTGACATCG	ATGCTGTGGA	1560
GCTGTATCCT	GCCCTTCTGG	TAGAAAAGCC	TCGGCCAGAT	GCCATCTTTG	GTGAAACCAT	1620
GGTAGAAGTT	GGAGCACCAT	TCTCCTTGAA	AGGACTTATG	GGTAATGTTA	TATGTTCTCC	1680
TGCCTACTGG	AAGCCAAGCA	CTTTTGGTGG	AGAAGTGGGT	TTTCAAATCA	TCAACACTGC	1740

Annotated Sheets Showing Changes

FIG. 2B

CTCAATTCAG	TCTCTCATCT	GCAATAACGT	GAAGGGCTGT	CCCTTTACTT	CATTCAGTGT	1800
TCCAGATCCA	GAGCTCATTA	AAACAGTCAC	CATCAATGCA	AGTTCTTCCC	GCTCCGGACT	1860
AGATGATATC	AATCCCACAG	TACTACTAAA	AGAACGGTCG	ACTGAACTGT	AGAAGTCTAA	1920
TGATCATATT	TATTTATTTA	TATGAACCAT	GTCTATTAAT	TTAATTATTT	AATAATATTT	1980
ATATTAAACT	CCTTATGTTA	CTTAACATCT	TCTGTAACAG	AAGTCAGTAC	TCCTGTTGCG	2040
GAGAAAGGAG	TCATACTTGT	GAAGACTTTT	ATGTCACTAC	TCTAAAGATT	TTGCTGTTGC	2100
TGTTAAGTTT	GGAAACAGT	TTTTATTCTG	TTTTATAAAC	CAGAGAGAAA	TGAGTTTTGA	2160
CGTCTTTTTA	CTTGAATTTC	AACTTATATT	ATAAGGACGA	AAGTAAAGAT	GTTTGAATAC	2220
TTAAACACTA	TCACAAAGATG	CCAAAATGCT	GAAAGTTTTT	ACACTGTCGA	TGTTTCCAAT	2280
GCATCTTCCA	TGATGCATTA	GAAGTAACTA	ATGTTTGAAA	TTTTAAAGTA	CTTTTGGGTA	2340
TTTTTCTGTC	ATCAAACAAA	ACAGGTATCA	GTGCATTATT	AAATGAATAT	TTAAATTAGA	2400
CATTACCAGT	AATTTTCATGT	CTACTTTTTA	AAATCAGCAA	TGAAACAATA	ATTTGAAATT	2460
TCTAAATTCA	TAGGGTAGAA	TCACCTGTAA	AAGCTTGTTT	GATTTCTTAA	AGTTATTAAA	2520
CTTGTAACATA	TACCAAAAAG	AAGCTGTCTT	GGATTTAAAT	CTGTAAAATC	AGATGAAATT	2580
TTACTACAAT	TGCTTGTTAA	AATATTTTAT	AAGTGATGTT	CCTTTTTTCAC	CAAGAGTATA	2640
AACCTTTTTA	GTGTGACTGT	TAAAACTTCC	TTTTAAATCA	AAATGCCAAA	TTTATTAAGG	2700
TGGTGAGGCC	ACTGCAGTGT	TATCTCAAAA	TAAGAAATATC	CTGTTGAGAT	ATTCCAGAAT	2760
CTGTTTATAT	GGCTGGTAAC	ATGTAAAAAC	CCCATAACCC	CGCCAAAAGG	GGTCC'TACCC	2820
TTGAACATAA	AGCAATAACC	AAAGGAGAAA	AGCCCAAATT	ATTGGTTCCA	AATTTAGGGT	2880
TTAAACTTTT	TGAAGCAAAC	TTTTTTTTTAG	CCTTGTCAC	TGCAGACCTG	GTACTCAGAT	2940
TTTGCTATGA	GGTTAATGAA	GTACCAAGCT	GTGCTTGAAT	AACGATATGT	TTTCTCAGAT	3000
TTTCTGTTGT	ACAGTTTAAT	TTAGCAGTCC	ATATCACATT	GCAAAAGTAG	CAATGACCTC	3060
ATAAAATACC	TCTTCAAAAT	GCTTAAATTC	ATTTACACACA	TTAATTTTAT	CTCAGTCTTG	3120
AAGCCAATTC	AGTAGGTGCA	TTGGAATCAA	GCCTGGCTAC	CTGCATGCTG	TTCTTTTTCT	3180
TTTCTTCTTT	TAGCCATTTT	GCTAAGAGAC	ACAGTCTTCT	CAAACACTTC	GTTTCTCCTA	3240
TTTTGTTTTA	CTAGTTTTTA	GATCAGAGTT	CACTTTCTTT	GGACTCTGCC	TATATTTTCT	3300
TACCTGAACT	TTTGCAAGTT	TTCAGGTAAA	CCTCAGCTCA	GGACTGCTAT	TTAGCTCCTC	3360
TTAAGAAGAT	TAAAAAATAA	AAAAAAG	(SEQ ID NO: 11)			3387